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=> file medline biosis caplus

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=> christer?/au

L1 369 CHRISTER?/AU

=> owman?/au

L2 1341 OWMAN?/AU

=> l1 and l2

L3 0 L1 AND L2

=> heptahelix

L4 25 HEPTAHELIX

=> l4 and receptor

L5 25 L4 AND RECEPTOR

=> leukotriene b4 receptor

L6 551 LEUKOTRIENE B4 RECEPTOR

=> l5 or l6

L7 575 L5 OR L6

=> l7 and 1970-1997/py

2 FILES SEARCHED...
L8 316 L7 AND 1970-1997/PY

=> dup rem 18

PROCESSING COMPLETED FOR L8
L9 198 DUP REM L8 (118 DUPLICATES REMOVED)

=> d his

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FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 16:11:23 ON 14 APR 2003

L1 369 CHRISTER?/AU
L2 1341 OWMAN?/AU
L3 0 L1 AND L2
L4 25 HEPTAHELIX
L5 25 L4 AND RECEPTOR
L6 551 LEUKOTRIENE B4 RECEPTOR
L7 575 L5 OR L6
L8 316 L7 AND 1970-1997/PY
L9 198 DUP REM L8 (118 DUPLICATES REMOVED)

=> logoff

ID P2Y7_HUMAN STANDARD; PRT; 352 AA.
AC Q15722; Q13305; Q92641;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE P2Y purinoceptor 7 (P2Y7) (Leukotriene B₄ receptor) (Chemoattractant receptor-like 1).
GN LTB4R OR P2RY7 OR GPR16 OR CMKRL1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96324902; PubMed=8702478;
RA Akbar G.K.M., Dasari V.R., Webb T., Ayyanathan K.,
RA Pillarisetti K., Sandhu A.K., Athwal R.S., Daniel J.L., Ashby B.,
RA Barnard E.A., Kunapuli S.P.,
RT "Molecular cloning of a novel P2 purinoceptor from human
erythroleukemia cells.",
RL J. Biol. Chem. 271:18363-18367(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96145150; PubMed=8558062;
RA Raport C.J., Schweickart V.L., Chantry D., Eddy R.L. Jr., Shows T.B.,
RA Godiska R., Gray P.W.;
RT "New members of the chemokine receptor gene family.",
RL J. Leukoc. Biol. 59:18-23(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97320501; PubMed=9177352;
RA Yokomizo T., Izumi T., Chang K., Takuwa Y., Shimizu T.,
RT "A G-protein-coupled receptor for leukotriene B₄ that mediates
chemotaxis.",
RL Nature 387:620-624(1997).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97079680; PubMed=8921391;
RA Owman C.S.O., Nilsson C., Lolait S.J.;
RT "Cloning of cDNA encoding a putative chemoattractant receptor.",
RL Genomics 37:187-194(1996).
CC -!- FUNCTION: RECEPTOR FOR EXTRACELLULAR ATP > UTP AND ADP. THE
CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
CC A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. MAY BE THE
CC CARDIAC P2Y RECEPTOR INVOLVED IN THE REGULATION OF CARDIAC MUSCLE
CC CONTRACTION THROUGH MODULATION OF L-TYPE CALCIUM CURRENTS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN HEART, SKELETAL
CC MUSCLE AND AT LOWER LEVELS IN BRAIN AND LIVER. HIGH LEVEL OF
CC EXPRESSION IN LYMPHOID TISSUES.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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DR EMBL; U41070; AAC50628.1; -.
DR EMBL; U33448; AAB16747.1; ALT_INIT.
DR EMBL; D89079; BAA20424.1; -.
DR EMBL; D89078; BAA20423.1; -.
DR EMBL; X98356; CAA67001.1; -.
DR Genew; HGNC:6713; LTB4R.
DR MIM; 601531; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR003983; LTB1_rec.
DR InterPro; IPR003981; LTB_rec.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PRINTS; PR01477; LTB1RECEPTOR.
DR PRINTS; PR01476; LTBRECEPTOR.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 19 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 20 42 1 (POTENTIAL).
FT DOMAIN 43 54 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 55 75 2 (POTENTIAL).
FT DOMAIN 76 91 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 92 113 3 (POTENTIAL).
FT DOMAIN 114 138 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 139 159 4 (POTENTIAL).
FT DOMAIN 160 178 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 179 199 5 (POTENTIAL).
FT DOMAIN 200 221 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 222 242 6 (POTENTIAL).
FT DOMAIN 243 268 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 269 289 7 (POTENTIAL).
FT DOMAIN 290 352 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 2 2 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 246 246 G -> R (IN REF. 4).
FT CONFLICT 272 272 A -> V (IN REF. 1).
FT CONFLICT 293 293 L -> V (IN REF. 1).
SQ SEQUENCE 352 AA; 37557 MW; 5A7BFC0A659AC81C CRC64;

Query Match 100.0%; Score 1749; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.1e-94;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNTTSSAAPP SLGVEFISLLAIILLSVALAVGLPGNSFVVWSILKRMQKRSVTALMVLNL 60
|||
Db 1 MNTTSSAAPP SLGVEFISLLAIILLSVALAVGLPGNSFVVWSILKRMQKRSVTALMVLNL 60

Qy 61 ALADLAVLLTAPFFLHFLAQGTWSFGLAGCRLCHYVCGVSMYASVLLITAMSLDRSLAVA 120
|||
Db 61 ALADLAVLLTAPFFLHFLAQGTWSFGLAGCRLCHYVCGVSMYASVLLITAMSLDRSLAVA 120

Qy 121 RPFVSQKLRTKAMARRVLAGIWVLSFLLATPVLAYRTVVPWKTNMSLCFPYR PSEGHR A F 180
|||
Db 121 RPFVSQKLRTKAMARRVLAGIWVLSFLLATPVLAYRTVVPWKTNMSLCFPYR PSEGHR A F 180

Qy 181 HLIFEAVTGFLLPFLAVVASYSDIGRRLQARRFRSRRTGRLVVLIIILTFAAFWLPYHVV 240
|||
Db 181 HLIFEAVTGFLLPFLAVVASYSDIGRRLQARRFRSRRTGRLVVLIIILTFAAFWLPYHVV 240

Qy 241 NLAEAGR ALAGQAAGLGLVGKRLSLARNV LIALAFLSSSVNPVLYACAGGGLLRSAGVGF 300
|||
Db 241 NLAEAGR ALAGQAAGLGLVGKRLSLARNV LIALAFLSSSVNPVLYACAGGGLLRSAGVGF 300

Qy 301 VAKLLEGTGSEASSTRRGSLGQTARSGPAALEPGPSELTASSPLKLNELN 352
|||
Db 301 VAKLLEGTGSEASSTRRGSLGQTARSGPAALEPGPSELTASSPLKLNELN 352

WEST Search History

DATE: Monday, April 14, 2003

| <u>Set Name</u> | <u>Query</u> | <u>Hit Count</u> | <u>Set Name</u> |
|-----------------|--------------|------------------|-----------------|
| side by side | | result set | |

DB=USPT; PLUR=YES; OP=AND

| | | | |
|----|-----------------------------------|----|----|
| L5 | l1 and L4 | 1 | L5 |
| L4 | leukotriene near b4 near receptor | 23 | L4 |
| L3 | leukotriene adj b4 adj receptor | 23 | L3 |
| L2 | heptahelix adj receptor | 4 | L2 |
| L1 | christer.in. and owman.in. | 3 | L1 |

END OF SEARCH HISTORY